Amendments to the Specification

The additions have been indicated by underlining (underlining).

Please replace the paragraph on page 17 lines 12-26 with the following amended paragraph:

Figure 1. HeLa cytoplasmic S100 extracts show siRNA-dependent target RNA cleavage.
(A) Representation of the 177-nt ^{32}P-cap-labeled target RNA [SEQ ID NO: 37] with the targeting siRNA duplex [sense siRNA: SEQ ID NO: 38; antisense siRNA: SEQ ID NO: 39]. Target RNA cleavage site and the length of the expected cleavage products is also shown. The fat black line positioned under the antisense siRNA is used in the following figures as symbol to indicate the region of the target RNA, which is complementary to the antisense siRNA sequence. (B) Comparison of the siRNA mediated target RNA cleavage using the previously established *D. melanogaster* embryo in vitro system and HeLa cell S100 cytoplasmic extract. 10 nM cap-labeled target RNA was incubated with 100 nM siRNA as described in materials. Reaction products were resolved on a 6% sequencing gel. Position markers were generated by partial RNase T1 digestion (T1) and partial alkaline hydrolysis (OH) of the cap-labeled target RNA. The arrow indicates the 5' cleavage product, the 3' fragment is unlabeled and therefore invisible.

Please replace the paragraph on page 18 lines 8-21 with the following amended paragraph:

Figure 3. siRNA containing 3'-terminal phosphates are subjected to ligation as well as dephosphorylation reactions.
(A) Sequence of the radiolabeled siRNA duplex [upper strand: SEQ ID NO: 40; lower strand: SEQ ID NO: 41]. The labeled nucleotide was joined to synthetic 20-nt antisense siRNA by T4 RNA ligation of ^{32}pCp. The various combinations of 5' and 3' hydroxyl/phosphate were prepared as described in materials. X and Y indicate 5' and 3' modifications of the antisense siRNA.

(B) Fate of the antisense siRNA during incubation of the modified siRNA duplexes in HeLa S100 extract in the presence of non-radiolabeled target RNA. The different phosphorylated forms of the antisense siRNA were distinguished based on their gel mobility. Identical results were obtained when using 5' phosphorylated sense siRNA or when leaving out the target RNA during incubation. Ligation products are only observed when 3' phosphates were present on the labeled antisense siRNA.

Please replace the table spanning page 21 lines 23-25 through page 24 line 1 with the following amended table:

Lane	Sense siRNA (5' – 3')	Antisense siRNA (5' – 3')
1		pUCGAAGUAUUCCG CG [SEQ ID NO: 1]
2		pUCGAAGUAUUCCG CGUACGUG [SEQ ID NO: 2]
3		pUCGAAGUAUUCCG CGUACGUGAUGU [SEQ ID NO: 3]
4		pUCGAAGUAUUCCG CGUACGUGAUGUUC [SEQ ID NO: 4]
5		pUCGAAGUAUUCCG CGUACGUGAUGUUC AC [SEQ ID NO: 5]

6		pUCGAAGUAUUCCG CG [SEQ ID NO: 6]
7		pUCGAAGUAUUCCG CGUACGUG [SEQ ID NO: 7]
8		pUCGAAGUAUUCCG CGUACGUGAUGU [SEQ ID NO: 8]
9		pUCGAAGUAUUCCG CGUACGUGAUGUUC [SEQ ID NO: 9]
10		pUCGAAGUAUUCCG CGUACGUGAUGUUC AC [SEQ ID NO: 10]
11		pUCGAAGUAUUCCG CGUACGUG [SEQ ID NO: 11]
12		pUCGAAGUAUUCCG CGUACGtg [SEQ ID NO: 12]
13		pUCGAAGUAUUCCG CGUACGUU [SEQ ID NO: 13]
14		pUCGAAGUAUUCCG CGUACGtt [SEQ ID NO: 14]

15		pUCGAAGUAUUCCG CGUACGUG [SEQ ID NO: 15]
16		pUCGAAGUAUUCCG CGUACGtg [SEQ ID NO: 16]
17		pUCGAAGUAUUCCG CGUACGUU [SEQ ID NO: 17]
18		pUCGAAGUAUUCCG CGUACGtt [SEQ ID NO: 18]
19	CGUACGCGGAAUACUUCG AAA [SEQ ID NO: 19]	pUCGAAGUAUUCCG CGUACGUG [SEQ ID NO: 20]
20	CGUACGCGGAAUACUUCG AAA [SEQ ID NO: 21]	pUCGAAGUAUUCCG CGUACGtg [SEQ ID NO: 22]
21	CGUACGCGGAAUACUUCG AAA [SEQ ID NO: 23]	pUCGAAGUAUUCCG CGUACGUU [SEQ ID NO: 24]
22	CGUACGCGGAAUACUUCG AAA [SEQ ID NO: 25]	pUCGAAGUAUUCCG CGUACGtt [SEQ ID NO: 26]
23		tCGAAGUAUUCCGC GUACGUULB [SEQ ID NO: 27]

24	cGUACGCGGAAUACUUCG AUULB [SEQ ID NO: 28]	tCGAAGUAUUCCGC GUACGUULB [SEQ ID NO: 29]
25		ptCGAAGUAUUCCGC GUACGttLB [SEQ ID NO: 30]
26	cGUACGCGGAAUACUUCG AttLB [SEQ ID NO: 31]	ptCGAAGUAUUCCGC GUACGttLB [SEQ ID NO: 32]
27		ptCGAAGUAUUCCGC GUACGttL [SEQ ID NO: 33]

Please replace the paragraph on page 24 lines 21-26 with the following amended paragraph:

Figure 13. Mass spectrometric characterization of eIF2C1 and eIF2C2.
The 100 kDa band was analysed by mass spectrometry. Mass spectrum indicating the peptide peaks corresponding to eIF2C2 (A) and eIF2C1 (B). (C) Alignment of eIF2C2 [SEQ ID NO: 69] and eIF2C1 [SEQ ID NO: 68] amino-acid sequences indicating the position of the identified peptides. Sequence differences are indicated by yellow boxes.

Please replace the paragraph on page 24 lines 28-29 with the following amended paragraph:

Figure 14. Predicted amino-acid sequences of the six human Argonaute protein family members [eIF2C1: SEQ ID NO: 68; eIF2C2: SEQ ID NO: 69; eIF2C3: SEQ ID NO: 70; eIF2C4: SEQ ID NO: 71; HILI: SEQ ID NO: 72; HIWI: SEQ ID NO: 73].

Please replace the paragraph on page 25 lines 1-4 with the following amended paragraph:

Figure 15. Alignment of the sequences of the six human Argonaute protein family members. [eIF2C1: SEQ ID NO: 68; eIF2C2: SEQ ID NO: 69; eIF2C3: SEQ ID NO: 70; eIF2C4: SEQ ID NO: 71; HILI: SEQ ID NO: 72; HIWI: SEQ ID NO: 73].
Predicted sequences of human eIF2C1-4, HILI and HIWI have been aligned using ClustalX program.

Please replace the paragraph on page 25 lines 6-7 with the following amended paragraph:

Figure 16. Predicted cDNA sequences of the six human Argonaute protein family members [eIF2C1: SEQ ID NO: 74; eIF2C2: SEQ ID NO: 75; eIF2C3: SEQ ID NO: 76; eIF2C4: SEQ ID NO: 77; HILI: SEQ ID NO: 78; HIWI: SEQ ID NO: 79].

Please replace the paragraph on page 37 lines 12-18 with the following amended paragraph:

Mass spectrometry analysis also revealed the presence of three peptides belonging exclusively to the HILI member of the Argonaute family of proteins. The sequences of those peptides are: NKQDFMDLSICTR [SEQ ID NO: 34], corresponding to positions 17-29 of the protein; TEYVAESFLNCLRR [SEQ ID NO: 35], corresponding to positions 436-449 of the protein, and;

YNHDLPARIIVYR [SEQ ID NO: 36], corresponding to positions 591-603 of the protein. This finding suggests that the protein HILI may also be part of RISC.